

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
- (ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4250 Executive Square, 7th Floor
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 28-NOV-2000
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 6869-402E
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 858-450-8403
(B) TELEFAX: 858-587-5360
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTNCCATGA	TTTAAAGTTT	60
TCTCGCCATA	TTCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTTC	AGTTTTCTCTC	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTCTGTC	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTTAAT	TTTCCACCTT	TTTCAATTTT	CACGCCATAT	480
TTTATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTT	ACTGATTTTC	TCATTTTTC	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTCAAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTTCAGTG	TTTCGTCATT	TTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCTT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCTTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTT	ACGTTTTTCA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAT	1080
GGATGTTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACAG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCACGTT	TTTCAGTGAA	TTC			1293

- (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAAC	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
AACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTGT	AAACCTTCAT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTCTGTTG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660

GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720
AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGTT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCCAGA	ATCTTGTTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	CCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGCG	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTAAAT	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTTGT	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGTCTCTTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAATTTT	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCATTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTTC	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAT	GCATCGTCTA	GTCCTACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280

TTGAATTTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340
CCGTCACACC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCCAT	CTGCCCCGAG	GTGGCGGCTG	2400
CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA	TTGGGATGTT	TCAGTTGA	28
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC	CCCTAGGAGA	TCTTAAGGA	29
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA	CTCTGATGAG	TCCGTGAGGA	CGAAACGCTC	TCGCACC
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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35				40						45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
		50				55					60					
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65				70					75					80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
			85					90					95			
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
		115					120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
		130				135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
145				150					155					160		
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165				170					175			
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624

Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro		
		195					200					205					
TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672	
Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg		
	210					215					220						
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	720	
Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val		
	225				230					235					240		
AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG	768	
Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met		
				245					250					255			
TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC	816	
Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly		
			260				265						270				
GCC	AAG	AAG	TTT	CCT	AAT	ACT	GAA	TTT	GTC	AAA	GTA	AAA	GGT	CTT	CAT	864	
Ala	Lys	Lys	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His		
		275					280					285					
TTT	TCG	CAA	GAA	GAT	GCA	CCT	GAT	GAA	ATG	GGA	AAA	TAT	ATC	AAA	TCG	912	
Phe	Ser	Gln	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser		
	290					295					300						
TTC	GTT	GAG	CGA	GTT	CTC	AAA	AAT	GAA	CAA	TAA						945	
Phe	Val	Glu	Arg	Val	Leu	Lys	Asn	Glu	Gln								
	305				310												

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGACTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAACATA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATTC	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAAC TAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTTCT	GAAGGTTTCT	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTTCTTC	ACTCCATGTG	CTCTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCTTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCCTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAAC TAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240

TTCCGGGATT	GCGTGTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTTC	TTCTTTGATT	GGTCTGTAAG	CTTAAGGCCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTCA	GCAGCCCAG	AGAGTTGCAC	720
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCTTCCCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTCAGGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCA	TTCGCCGTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	1080
GGTGGTTCTT	CACCTCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAAT	TCTCCTTAAT	AGGGACGGGG	1200
TTTCGTTTTC	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCCTGAAGA	1260
TGTAAGAATA	AAGCTTTGCC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGGTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAACG	TGCGTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTTCACT	60
ACAAC TGCCA	CGAGGCCCGG	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTTGCCA	180
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACTCATTGC	CAGACACAGG	TGCCCACCTT	240
TGGCATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGATAT	360
ACCTAATAAA	AATTAATAA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAA	TTATTTCACT	420
AATTTATTTT	CTTTCTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCTTTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACCTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTTCCCTTGA	AACTCAGGAT	CAAATTCAGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTAC	840
CAGTGCCCTC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	900
GTGAAC TGGT	CATTCACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTTCGAGA	TAGAAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CCTAGACCTT	TTCTTCACCT	TTATTAAATA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	1140
TACGGATGTT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CAC TTATTGG	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAT	1260
ATTAAACATC	AGTCCCAAAT	TACAACTTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	GCGTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCCT	ATCCCTAATC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCATTA	60
AAAACCTGT	AGGATCTTCA	CTCTAGGTCA	CTGTTTCAGCA	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCACTCT	GGCCATAATT	ATTGAGGACG	TTGATTTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCTGTC	TGTCTGTCTG	TCTGTCTGTC	TATCAAACCA	AAAGAAACCA	AACAATTATG	360
CCTGCCTGCC	TGCCTGCCTG	CCTACACAGA	GAAATGATTT	CTTCAATCAA	TCTAAAACGA	420
CCTCCTAAGT	TTGCCCTTTT	TCTCTTTCTT	TATCTTTTTC	TTTTTTCTTT	TCTTCTTCTT	480
TCCTTCTTCT	CTTCTTCTCT	TCCTTCTTCT	CTTCTTCTCT	TTCTTTCTTT	CTTACTTTCT	540
TTCTTTCTCT	CTTACATTTA	TTCTTTTTCAT	ACATAGTTTC	TTAGTGTAAG	CATCCCTGAC	600
TGTCTTGAAG	ACACTTTTGT	GGCCTCAATC	CTGTAAGAGC	CTTCCTCTGC	TTTTCAAATG	660
CTGGCATGAA	TGTTGTACCT	CACATGACC	AGCTTAGTCT	TCAAGTCTGA	GTTACTGGAA	720
AGGAGTTCCA	AGAAGACTGG	TTATATTTT	CATTTATTAT	TGCATTTTAA	TTAAAATTTA	780
ATTTACCAA	AAGAATTTAG	ACTGACCAAT	TCAGAGTCTG	CCGTTTAAAA	GCATAAGGAA	840
AAAGTAGGAG	AAAAACGTGA	GGCTGTCTGT	GGATGGTCGA	GGCTGCTTTA	GGGAGCCTCG	900
TCACCATTCT	GCACTTGCAA	ACCGGGCCAC	TAGAACCCGG	TGAAGGGAGA	AACCAAAGCG	960
ACCTGGAAAC	AATAGGTCAC	ATGAAGGCCA	GCCACCTCCA	TCTTGTTGTG	CGGGAGTTCA	1020
GTTAGCAGAC	AAGATGGCTG	CCATGCACAT	GTTGTCTTTC	AGCTTGGTGA	GGTCAAAGTA	1080
CAACCGAGTC	ACAGAACAAG	GAAGTATACA	CAGTGAGTTC	CAGGTCAGCC	AGAGTTTACA	1140
CAGAGAAACC	ACATCTTGAA	AAAAACAAAA	AAATAAATTA	AATAAATATA	ATTTAAAAAT	1200
TTAAAAATAG	CCGGGAGTGA	TGGCGCATGT	CTTTAATCCC	AGCTCTCTTC	AGGCAGAGAT	1260
GGGAGGATTT	CTGAGTTTGA	GGCCAGCCTG	GTCTGCAAAG	TGAGTTCAG	GACAGTCAGG	1320
GCTATACAGA	GAAACCCGTG	CTTGAAAAC	AAACTAAAT	AAACTAAACT	AAACTAAAAA	1380
AATATAAAAT	AAAAATTTTA	AAGAATTTTA	AAAAACTACA	GAAATCAAAC	ATAAGCCCAC	1440
GAGATGGCAA	GTAAGTGC	TCATAGCAGA	AATATTATAC	ACACACACAC	ACACAGACTA	1500
TGTCATAAAA	TCCAATGTGC	CTTCATGATG	ATCAAATTTT	GATAGTCAGT	AATACTAGAA	1560
GAATCATATG	TCTGAAAATA	AAAGCCAGAA	CCTTTTCTGC	TTTTGTTTTT	TTTTGCCCCA	1620
AGATAGGGTT	TCTCTCAGTG	TATCCCTGGC	ATCCCTGCCT	GGAACCTTCT	TTGTAGGTTT	1680
GGTAGCCTCA	AACTCAGAGA	GGTCTCTCT	GCCTGCCTGC	CTGCCTGCCT	GCCTGCCTGC	1740
CTGCCTGCCT	GCCTGCCTCA	CTTCTTCTGC	CACCCACACA	ACCGAGTCGA	ACCTAGGATC	1800
TTTATTTCTT	TCTCTTCTCT	TCTTCTTCTT	TTCTTTCTTT	CTTTCTTTCT	TTCTTTCTTT	1860
CTTCTTTCT	TTCTTTATCA	ATTAGTTTTC	AATGTAAGTG	TGTGTTTGTG	CTCTATCTGC	1920
TGCCTATAGG	CCTGCTTGCC	AGGAGAGGGC	AACAGAACCT	AGGAGAAACC	ACCATGCAGC	1980
TCCTGAGAAT	AAGTGAAAAA	ACAACAAAAA	AAGGAAATTC	TAATCACATA	GAATGTAGAT	2040
ATATGCCGAG	GCTGTCAGAG	TGCTTTTAA	GGCTTAGTGT	AAGTAATGAA	AATTGTTGTG	2100
TGCTTTTAT	CCAAACACAG	AAGAGAGGTG	GCTCGGCTG	CATGTCTGTT	GTCTGCATGT	2160
AGACCAGGCT	GGCCTTGAAC	ACATTAATCT	GTCTGCCTCT	GCTTCCCTAA	TGCTGCGATT	2220
AAAGGCATGT	GCCACCACTG	CCCGGACTGA	TTTCTTCTTT	TTTTTTTTTT	TGGAAAATAC	2280
CTTTCTTTCT	TTTCTCTCT	CTCTTCTTCT	CTTCTTCTCT	TTCTTTCTAT	TCTTTTTTTC	2340
TTTCTTTTTT	CTTTTTTTTT	TTTTTTTTTAA	AATTTGCCTA	AGGTTAAAGG	TGTGCTCCAC	2400
AATTGCCTCA	GCTCTGCTCT	AATTCTCTTT	AAAAAAAAAAC	AAACAAAAAA	AAAACCAAAA	2460
CAGTATGTAT	GTATGTATAT	TTAGAAGAAA	TACTAATCCA	TTAATAACTC	TTTTTTTCTA	2520
AAATTCATGT	CATTCTTGTT	CCACAAAGTG	AGTTCCAGGA	CTTACCAGAG	AAACCTGTG	2580
TTCAAATTTT	TGTGTTCAAG	GTCACCCCTGG	CTTACAAAGT	GAGTTCCAAG	TCCGATAGGG	2640
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAAGTTCC	AAACACACAC	ACACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	CGCGCCGCGG	CGATGAGGGG	2760
AAGTCGTGCC	TAAAATAAAT	ATTTTTCTGG	CCAAAGTGAA	AGCAAATCAC	TATGAAGAGG	2820
TACTCCTAGA	AAAAATAAAT	ACAAACGGGC	TTTTTAATCA	TTCCAGCACT	GTTTTAATTT	2880
AACCTCTGAAT	TTAGTCTTGG	AAAAGGGGGG	GGGTGTGGGT	GAGTGAGGGC	GAGCGAGCAG	2940
ACGGGCGGGC	GGGCGGGTGA	GTTGGCCGGC	GCGGTGGCAG	CGAGCACCAG	AAAACAACAA	3000
ACCCCAAGCG	GTAGAGTGTT	TTAAAAATGA	GACCTAAATG	TGGTGGAACG	GAGGTGCGCC	3060
CCACCTCTCT	CTTCCACTGC	TTAGATGCTC	CCTTCCCCTT	ACTGTGCTCC	CTTCCCCTAA	3120
CTGTGCCTAA	CTGTGCCTGT	TCCCTCACCC	CGCTGATTGC	CCAGCGACGT	ACTTTGACTT	3180

CAAGAACGAT	TTTGCCTGTT	TTCACCGCTC	CCTGTGCATAC	TTTCGTTTTT	GGGTGCCCGA	3240
GTCTAGCCCC	TTTCGCTATGT	TCGGGCGGGA	CGATGGGGAC	CGTTTGTGCC	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGCCTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCTCCG	GAGAGACAGA	ATGAGTGAGT	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTGTATG	GTTGATCGAG	ACCATTTGTCG	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCCTGTGG	TGAGGCGACC	3540
AGGGTGACAG	GAGGCCGGGC	AAGCAGGCGG	GAGCGTCTCG	GAGATGGTGT	CGTGTTTAAG	3600
GACGGTCTCT	AACAAGGAGG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTTGCTGTAC	3660
GCCCTTTTGG	GAAAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTGCGACC	AGAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTTT	TTTCTCTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGG	ACCGTACATC	TGAGGCCGAG	AGGACGCGAT	GGGCCCCGGT	TCCAAGCCGG	3840
TGTGGCTCGG	CCAGCTGGCG	CTTCGGGTCT	TTTTTTTTTT	TTTTTTTTTT	TTTTCTCTCA	3900
GAAGCCTTGT	CTGTCGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCGAG	AGGACGCGAT	3960
GGGCCCCGGC	TTCCAAGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGTC	TTTTTTTTTT	4020
TTTTTTTTTT	TTTTTTTCTC	CAGAAGCCTT	GTCTGTGCGT	GTCACCGGGG	GCGCTGTACT	4080
TCTGAGGCCG	AGAGGACGCG	ATGGGTTCGGC	TTCCAAGCCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGTT	TTTTTTTTTT	CTCCAGAAGC	CCTCTCTTGT	CCCCGTCACC	GGGGGCGCTG	4200
TACTTCTGAG	GCCGAGAGGA	CGTGATGGGC	CCGGGTTCCA	GGCGGATGTC	GCCCGGTCAG	4260
CTGGAGCTTT	GGATCTTTTT	TTTTTTTTTT	CCTCCAGAAG	CCCTCTCTTG	TCCCCGTCAC	4320
CGGGGGCACC	TTACATCTGA	GGGCGAGAGG	ACGTGATGGG	TCCGGCTTCC	AAGCCGATGT	4380
GGCGGGGCTA	GCTGGAGCTT	CGGGTTTTTT	TTTTTTCCTC	CAGAAGCCCT	CTCTTGTCCC	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCC	GGTTCAGGC	4500
GGATGTCGCC	CGGTACAGCTG	GAGCTTTGGA	TCATTTTTTT	TTTTCCCTCC	AGAAGCCCTC	4560
TCTTGTCCCC	GTCACCGGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCGCTGT	4620
CTTCCAAGCC	GATGTGGCCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	TTTTTCTCTC	4680
CAGAAGCCTT	GTCGTGCTGT	GTCACCGGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740
ATGGGCCCCG	CTTCCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	4800
TTTTTTTTTT	TTCTCTCCAG	AACCTTGTCT	GTGCTGTGCA	CCCGGGGCGC	TTGTACTTCT	4860
GATGCCGAGA	GGACGCGATG	GGCCCCGTCT	CCAGGCCGAT	GTGGCCCCGG	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTTT	TTTTCTCTCA	GAAGCCCTCT	CTTGTCCCCG	TCACCGGGGG	4980
CACCTTACAT	CTGAGGCCTA	GAGGACACGA	TGGGCCCGGG	TTCCAGGCCG	ATGTGGCCCC	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTTT	TTTTCTTCCA	GAAGCCCTCT	TGTCCCCGTC	5100
ACCGGTGGCA	CTGTACATCT	GAGGCGGAGA	GGACATTATG	GGCCCCGGCT	CCAATCCGAT	5160
GTGGCCCCGT	CAGCTGGAGC	TTTGGATCTT	ATTTTTTTTT	TAATTTTTTT	TTCCAGAAGC	5220
CCTCTTGTCC	CTGTCACCGG	GTCACCGGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCCC	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCAGCT	GGAGCTTTGG	ATCTTTTTTT	TTTTTTTTTCT	5340
TTTTTCTCTC	AGAAGCCCTC	TCTGTCCCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTTCTTTTAT	TGACCTGTCT	GTCTTATCAG	TTCTCCGGGT	5460
TGTGAGGGTC	GACCAAGTTG	TCCCTTTGAG	TCCGGTTCTT	TTCTGTTATG	GGTCAATTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTTGCTC	GCCTGTCACT	TTCTCCCTCT	5580
TCTCTTTTAT	GCTTGTGATC	TTTTCTATCT	GTTCTTATTG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AACACTAAAG	GACACTATAA	AGAGACCCCT	TCGATTTAAG	5700
GCTGTTTTGC	TTGTCCAGCC	TATTTCTTTT	ACTGGCTTGG	GTCTGTGCGG	GTGCTTGAAG	5760
CTGTCCCCGA	GCCACGCTTC	CTGCTTTCCC	GGGCTTGCTG	CTTGCCTGTG	CTTGCCTGTG	5820
GCAGCTTGTG	ACAACCTGGG	GCTGTGACTT	TGCTGCGTGT	CAGACGTTTT	TCCCGATTTT	5880
CCCGAGGTGT	CGTTGTACAC	CCTGTCCCGG	TTGGAATGGT	GGAGCCAGCT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGGCTCAC	TTTTTTTTTT	TTTTTTTTCT	TTGGAGTCCC	GAACCTCCGC	6000
TCTTTTCTCT	TCCCGGTCTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTCTT	TTTGTTTTTT	6060
TTCTTTTTTT	TTTTTTTTTT	TTGGGGAGGT	GGAGAGTCCC	GAGTACTTCA	CTCCTGTCTG	6120
TGGTGTCCAA	GTGTTTCATG	CACGTGCCTC	CCGAGTGCAC	TTTTTTTTTGT	GGCAGTCGCT	6180
CGTTGTGTTT	TCTTGTCTGT	TGTCTGCCCC	TATCAGTAAC	TGTCTTGCCC	CGCGTGTAA	6240
ACATTCTTAT	CTCGCTTGTT	TCTCCCGATT	GCGCGTCTGT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCGG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCGAGGG	ACGGACATTC	6360
ATGGCGAATG	GCGGCCGCTC	TTCTCGTTCT	GCCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCGG	TGGTGTGTGG	AAGGCAGGGG	TGCGGCTCTC	CGGCCCCGAC	CTGCCCCGCG	6480
CGCACTTTTC	TCAGTGGTTC	GCGTGGTCCT	TGTGGATGTG	TGAGGCGCCC	GGTTGTGCCC	6540
TCACGTGTTT	CACTTTGGTC	GTGTCTCGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGTGGCGGT	TGCATACCTT	TCCCGTCTGG	TGTGTGCACG	CGCTGTTTCT	TGTAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTTGTG	TCCTAGGTGC	CTGCTTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCTCCGGT	GCTCCGCTCT	GCTGTGTGCC	TTCCCGTTTG	6780
TGTCTGAGAA	GCCCCGTGAG	GGGGGGTCTG	GGAGAGAAGG	AGGGGCAAGA	CCCCCTTCT	6840
TCGTGCGGTG	AGGCGCCAC	CCCGCAGCTA	GTACGCTGT	GCGTAGGGCT	GGTGCTGAGC	6900
GTCGCGGCT	GGGGTTGGAA	AGTTTCTCGA	GAGACTCATT	GCTTTCCCGT	GGGGAGCTTT	6960
GAGAGGCCTG	GCTTTCGGGG	GGGACCGGTT	GCAGGGTCTC	CCCTGTCCGC	GGATGCTCAG	7020
AATGCCCTTG	GAAGAGAACC	TTCCTGTTGC	CGCAGACCCC	CCCGCGCGGT	CGCCGCGGTG	7080

TTGGTCTTCT	GTTTCCCTG	TGTGCTCGTC	GCATGCATCC	TCTCTCGGTG	GCCGGGGCTC	7140
GTCGGGGTTT	TGGGTCCGTC	CCGCCCTCAG	TGAGAAAGTT	TCCTTCTCTA	GCTATCTTCC	7200
GGAAAGGGTG	CGGGCTTCTT	ACGGTCTCGA	GGGGTCTCTC	CCGAATGGTC	CCCTGGAGGG	7260
CTCGCCCCCT	GACCGCCTCC	CGCGCGCGCA	GCGTTTGCTC	TCTCGTCTAC	CGCGGCCCGC	7320
GGCCTCCCCG	CTCCGAGTTC	GGGGAGGGAT	CACGCGGGGC	AGAGCCTGTC	TGTCGTCCGT	7380
CCGTTGCTGC	GGAGCATGTG	GCTCGGCTTG	TGTGGTTGGT	GGCTGGGGAG	AGGGCTCCGT	7440
GCACACCCCC	GCGTGC GCGT	ACTTTCCTCC	CCTCCTGAGG	GCCGCCGTGC	GGACGGGGTG	7500
TGGGTAGGCG	ACGGTGGGCT	CCCGGGTCCC	CACCCGTCTT	CCCGTGCCTC	ACCCGTGCCT	7560
TCCGTCGCGT	GCGTCCCTCT	CGCTCGCGTC	CACGACTTTG	GCCGCTCCCG	CGACGGCGGC	7620
CTGCGCCGCG	CGTGGTGCGT	GCTGTGTGCT	TCTCGGGCTG	TGTGGTTGTG	TCGCCTCGCC	7680
CCCCCTTCC	CGCGGCAGCG	TTCCACGGC	TGGCGAAATC	GCGGGAGTCC	TCCTTCCCCT	7740
CCTCGGGGTC	GAGAGGGTCC	GTGTCTGGCG	TTGATTGATC	TCGCTCTCGG	GGACGGGACC	7800
GTTCTGTGGG	AGAACGGCTG	TTGGCCGCGT	CCGGCGCGAC	GTCGGACGTG	GGGACCCACT	7860
GCCGCTCGGG	GGTCTTTCGT	GGTAGGCATC	GGTGTGTGCG	CATCGGTCTC	TCTCTCGTGT	7920
CGGTGTCGCC	TCCTCGGGCT	CCCGGGGGGC	CGTCGTGTTT	CGGGTCGGCT	CGGCGCTGCA	7980
GGTGTGGTGG	GACTGCTCAG	GGGAGTGGTG	CAGTGTGATT	CCCGCCGGTT	TTGCCTCCGG	8040
TGCCCTGACC	GGTCCGACGC	CCGAGCGGTC	TCTCGGTCCC	TTGTGAGGAC	CCCCTTCGGG	8100
GAGGGGCCCC	TTTCGGCCGC	CCTTGCCGTC	GTCGCCGGCC	CTCGTTCTGC	TGTGTGCTTC	8160
CCCCCTCCCC	GCTCGCCGCA	GCCGGTCTTT	TTTCTCTCT	CCCCCCTCT	CCTCTGACTG	8220
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 TTGTGGGGCT GGGGATCAGG TATCTCAACG GAATGCATGA AGGTTAAGGT GAGATGGCTC 21060
 GATTTTGTGA AAGATTACTT TTCTTAGTCT GAGGAAAAAA TAAAATAATA TTGGGCTACG 21120
 TTTTATTGCT TCATTTCTAT TTCTCTTTCT TTCTTTCTTT CTTTCAGATA AGGAGGTCGG 21180
 CCAGTTCCCT CTGCCTTCTG GAAGATGTAG GCATTGCATT GGGAAAAGCA TTGTTTGAGA 21240
 GATGTGCTAG TGAACCAGAG AGTTTGGATG TCAAGCCGTA TAATGTTTAT TACAATATAG 21300
 AAAAGTTCTA ACAAAGTGAT CTTTAACTTT TTTTTTTTTT TTTCTCCTTC TACTTCTACT 21360
 TGTCTCACT CTGCCACCAA CGCGCTTTGT ACATTGAATG TGAGCTTTGT TTTGCTTAAC 21420
 AGACATATAT TTTTCTTTT GGTTTTGCTT GACATGGTTT CCCTTTCTAT CCGTGCAGGG 21480
 TTCCAGACG GCCTTTTGAG AATAAAATGG GAGGCCAGAA CCAAAGTCTT TTGAATAAAG 21540
 CACCACAACCT CTAACCTGTT TGGCTGTTTT CCTTCCCAAG GCACAGATCT TTCCAGCAT 21600
 GGAAAAGCAT GTAGCAGTTG TAGGACACAC TAGACGAGAG CACCAGATCT CATTTGTTGGT 21660
 GGTGTGAAC CACCCACCAT GTGGTTGCCT GGGATTTGAA CTCAGGATCT TCAGAAGACG 21720
 AGTCAGGGCT CTAAACCGAT GAGCCATCTC TCCAGCCCTC CTACATTCTT TCTTAAGGCA 21780
 TGAATGATCC CAGCATGGGA AGACAGTCTG CCTCTTTGT GGTATATCAC CATATACTCA 21840
 ATAAAATAAT GAAATGAATG AAGTCTCCAC GTATTTATTT CTTGAGCTA TCTAAATCT 21900
 CTCACAGCAC CTCCTCCCTC CCCACACTGC CTTTCTCCCT ATGTTTGGGT GGGGCTGGGG 21960
 GAGGGGTGGG GTGGGGGCAG GGATCTGCAT GTCTTCTTGC AGGTCTGTGA ACTATTTGCG 22020
 ATGGCCTGGT TCTCTGAAC GTTGAGCCTT GTCTATCCAG AGGCTGACTG GCTAGTTTTT 22080
 TACCTGAAGT CCCTGAGTGA TGATTTCCCT GTGAATTC 22118

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCTCTGG	CGACCTGTCTG	TCGGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
GGGCTCTGGC	CTCACGGTGA	CCGGCTAGCC	GGCCGCGCTC	CTGCCTTGAG	CCGCCTGCCG	120
CGGCCCCGGG	GCCTGTCTGT	CTCTCGCGCG	TCCGAGCGTC	CCGACTCCCC	GTGCCGGCCC	180
GGGTCCGGGT	CTCTGACCCA	CCCGGGGGCG	CCGGGTCCGA	CGGCGAGGGC	CACCGTGCCC	240
CGTGCGCTCT	CCGCTGCGGG	CGCCCCGGGC	GCCGCACAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCGTGTC	AGGCGTTCTC	GTCTCCGCGG	GGTTGTCCGC	CGCCCCCTTC	CCGGAGTGGG	360
GGGTGGCCGG	AGCCGATCGG	CTCGCTGGCC	GGCCGGCCTC	CGCTCCCGGG	GGGCTCTTCG	420
ATCGATGTGG	TGACGTCTGT	CTCTCCCGGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGGCG	480
GACGTTCTGT	GCGAACGGGA	CCGTCTTCT	CGCTCCGCC	GCGCGGTCCC	CTCGTCTGCT	540
CCTCTCCCCG	CCCGCCGGCC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCGACC	600
TCGCCGTCCC	GCCCCCGGCC	TTCGCTTCGC	GGGTGCGGGC	CGGCGGGGTC	CTCTGACGCG	660
GCAGACAGCC	CTGCCTGTCT	CCTCCAGTGG	TTGTGCACTT	GCGGGCGGGC	CCCCCTCCGC	720
GCGGTGGGGG	TGCCGTCCCG	CCGGCCCGTC	GTGCTGCCCT	CTCGGGGGGG	GTTTGCGCGA	780
GCGTCGGCTC	CGCCTGGGCC	CTTGCGGTGC	TCCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCCAGGCC	GAACGGTGGT	GTGTCTGTTC	CGCCCCCGGC	GCCCCCTCCT	CCGGTCGCCC	900
CCGCGGTGTC	CGCGCGTGGG	TCCTGAGGGA	GCTCGTCCGT	GTGGGGTTTC	AGGCGGTTTG	960
AGTGAGACGA	GACGAGACGC	GCCCCCTCCA	CGCGGGGAAG	GGCGCCCGCC	TGCTCTCGGT	1020
GAGCGCACGT	CCCGTGCTCC	CCTCTGGCGG	GTGCGCGCGG	GCCGTGTGAG	CGATCGCGGT	1080
GGGTTCGGGC	CGGTGTGACG	CGTGCGCCCG	CCGCCCGCCG	AGGGGCTGCC	GTTCTGCCTC	1140
CGACCGGTCT	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCC	TCGGAAGGAA	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTGCGCGCA	CGCGCGCACC	GGCCGGGCCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	GCGCGCAGGT	GTTTCCTCGT	ACCGCAGGGC	CCCCCTCCCTT	1320
CCCCAGGCGT	CCCTCGGCGC	CTCTGCGGGC	CCGAGGAGGA	GCGGCTGGCG	GGTGGGGGGA	1380
GTGTGACCCA	CCCTCGGTGA	GAAAAGCCTT	CTCTAGCGAT	CTGAGAGGCG	TGCTTTGGGG	1440
GTACCGGATC	CCCCGGGGCC	CCGCCTCTGT	CTCTGCCTCC	GTTATGGTAG	CGCTGCCGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCCG	TTCCCCCTCG	ACGGGGTTGG	GGGGGAGAAG	1560
CGAGGGTTCC	GCCGGCCACC	GCGGTGGTGG	CCGAGTCCGG	CTCGTCGCCT	ACTGTGGCCC	1620
GCGCCTCCCC	CTTCCGAGTC	GGGGGAGGAT	CCCGCCGGGC	CGGGCCCGGC	GCTCCCACCC	1680
AGCGGGTTGG	GACGCGGCGG	CCGGCGGGCG	GTGGGTGTGC	GCGCCCGGCG	CTCTGTCCCG	1740
CGCGTGACCC	CCTCCGTCCG	CGAGTCCGGT	CTCCGCCCGC	TCCCGTGCCG	AGTCGTGACC	1800
GGTGCCGACG	ACCGCGTTTG	CGTGGCACGG	GTCGCGGCC	GCCTGGCCCT	GGGAAAGCGT	1860
CCCACGGTGG	GGGCGCGCCG	GTCTCCCGGA	GCGGGACCGG	GTCGGAGGAT	GGACGAGAAT	1920
CACGAGCGAC	GGTGGTGGTG	GCGTGTCCGG	TTCTGTGGCT	CGGTCTGCTC	GGGGCCCCCG	1980
GTGGCGGGGC	CCCGGGGGCT	GCGAGGCGGT	TCTCGGTGGG	GGCCGAGGGC	CGTCCCGCGT	2040
CCCAGCCGGG	GCGCCGCGGG	ACCGCCCTCG	TGTCTGTGGC	GGTGGGATCC	CGCGGCCGTG	2100
TTTTCCTGGT	GGCCCGGCCG	TGCTGAGGT	TTCTCCCCGA	GCCCGCCGCT	CTGCGGGCTC	2160
CCGGGTGCCC	TTGCCCCTCG	GGTCCCCGGC	CCTCGCCCGT	CTGTGCCCTC	TTCCCCGCCC	2220
GCCGCCCGCC	GATCCTCTTC	TTCCCCCGCA	GCGGCTCACC	GGCTTCACGT	CCGTTGGTGG	2280
CCCCGCTTGG	GACCGAACCC	GGCACCGCCT	CGTGGGGCGC	CGCCGCCGGC	CACTGATCGG	2340
CCCCGGCTTC	GCGTCCCCCG	GCGCGCGCCT	TGGGGACCGG	GTCGGTGCGG	CGCCGCCTGG	2400
GGCCCGGTGG	GCTTCCCGGA	GGGTTCGCGG	GGTCGGCCTG	CGGCGCGTGC	GGGGGAGGAG	2460
ACGGTTCCGG	GGGACCGGCC	GCGGCTGCGG	CGGCGGCGGT	GGTGGGGGGA	GCCGCGGGGA	2520
TCGCCGAGGG	CCGCTCGGCC	GCCCCGGGTG	CCCCGCGGTG	CCGCCGGCGG	CGGTGAGGCC	2580
CCGCGCGTGT	GTCCCCGGTG	CGGTTCGGCG	CGCTCGAGGG	GTCCCCGTGG	CGTCCCCCTC	2640
CCCGCCGGCC	GCCTTCTTCG	CGCCTTCCCC	GTCGCCCCGG	CCTCGCCCGT	GGTCTCTCGT	2700
CTTCTCCCGG	CCCGCTCTTC	CGAACCGGGT	CGGCGCGTCC	CCCGGGTGCG	CCTCGCTTCC	2760
CGGGCCTGCC	GCGGCCCTTC	CCCGAGGCGT	CCGTCCCCGG	CGTCGGCGTC	GGGGAGAGCC	2820
CGTCTTCCCC	GCGTGGCGTC	GCCCCGTTCG	GCGCGCGCGT	GCGCCCGAGC	GCGGCCCGGT	2880
GGTCCCTCCC	GGACAGGCGT	TCGTGCGACG	TGTGGCGTGG	GTCGACCTCC	GCCTTGCCGG	2940
TCGCTCGCCC	TCTCCCCGGG	TCGGGGGGTG	GGGCCCCGGC	CGGGGCCCTC	GCCCCGGTCG	3000
CTGCCTCCCC	TCCCGGGCGG	GGGCGGGCGC	GCCGGCCGGC	CTCGGTTCGC	CTCCCTTGGC	3060
CGTCGTGTGG	CGTGTGCCAC	CCCTGCGCCG	GCGCCCGCCG	GCGGGGCTCG	GAGCCGGGCT	3120
TCGGCCGGGC	CCCGGGCCCT	CGACCGGACC	GGTTCGCGCT	GCGCTGCGGC	CGCACGGCGC	3180
GACTGTCCCC	GGGCCGGGCA	CCGCGGTCCG	CCTCTCGCTC	GCCGCCCGGA	CGTCGGGGCC	3240
GCCCCGCGGG	GCGGGCGGAG	CGCCGTCCCC	GCCTCGCCGC	CGCCCGCGGG	CGCCGGCCGC	3300
GCGCGCGCGC	GCGTGGCCGC	CGGTCCCTCC	CGGCCGCCGG	GCGCGGGTTC	GGCCGTCCGC	3360
CTCCTCGCGG	GCGGGCGCGA	CGAAGAAGCG	TCGCGGGTCT	GTGGCGCGGG	GCCCCCGGTG	3420

GTCGTGTCGC	GTGGGGGGCG	GGTGGTTGGG	GCGTCCGGTT	CGCCGCGCCC	CGCCCCGGCC	3480
CCACCGGTCC	CGGCCGCGCC	CCCCGCGCCC	GCTCGCTCCC	TCCCGTCCGC	CCGTCCGCGG	3540
CCCGTCCGTC	CGTCCGTCCG	TCGTCTCTCT	CGCTTGCGGG	GCGCCGGGGC	CGTCTCTCGC	3600
AGGCCCCCGG	GCCGGCCGTC	CGGCCGCGTC	GGGGGCTCGC	CGCGCTCTAC	CTTACCTACC	3660
TGGTTGATCC	TGCCAGTAGC	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGTCTAAGTA	3720
CGCACGGCCG	GTACAGTGAA	ACTGCGAATG	GCTCATTAAA	TCAGTTATGG	TTCCTTTGGT	3780
CGCTCGCTCC	TCTCTACTTT	GGATAACTGT	GGTAATTCTA	GAGCTAATAC	ATGCCGACGG	3840
GCGCTGACCC	CCTTCGCGGG	GGGGATGCGT	GCATTTATCA	GATCAAAAACC	AACCCGGTCA	3900
GCCCCCTCTC	GGCCCCGGCC	GGGGGGCGGG	CGCCGGCGGC	TTTGGTGAAT	CTAGATAACC	3960
TCGGGGCCGAT	CGCACGCCCC	CCGTGCGCGC	GACGACCCAT	TCGAACGTCT	GCCCTATCAA	4020
CTTTTCGATG	TAGTCGCCGT	GCCTACCATG	GTGACCACGG	GTGACGGGGA	ATCAGGGTTC	4080
GATTCCGGAG	AGGGAGCCTG	AGAAACGGTG	ACCACATCCA	AGGAAGGCAG	CAGGCGCGCA	4140
AATTACCCAC	TCCCGACCCG	GGGAGGTAGT	GACGAAAAAT	AACAATACAG	GACTCTTTTCG	4200
AGGCCCTGTA	ATTGGAATGA	GTCCACTTTA	AATCCTTTAA	CGAGGATCCA	TTGGAGGGCA	4260
AGTCTGGTGC	CAGCAGCCGC	GGTAATTCCA	GCTCCAATAG	CGTATATTAA	AGTTGCTGCA	4320
GTTAAAAAGC	TCGTAGTTGG	ATCTTGCGAG	CGGGCGGGCG	GTCCGCGCGC	AGGCGAGCCA	4380
CCGCCCCGTC	CCGCCCCCTG	CCTCTCGGCG	CCCCCTCGAT	GCTCTTAGCT	GAGTGTCCCG	4440
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ACCAAAGTCT	TTGGGTTCCG	GGGGGAGTAT	GGTTGCAAAAG	CTGAAACTTA	AAGGAATTGA	4860
CGGAAGGGCA	CCACCAGGAG	TGGAGCCTGC	GGCTTAATTT	GACTCAACAC	GGGAAACCTC	4920
ACCCGGCCCC	GACACGGACA	GGATTGACAG	ATTGATAGCT	CTTTCTCGAT	TCCGTGGGTG	4980
GTGGTGATGC	GCCGTTCTTA	GTTGGTGGAG	CGATTTGTCT	GGTTAATTCC	GATAACGAAC	5040
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TAGATGTCCG	GGGCTGCACG	CGCGCTACAC	TGACTGGCTC	AGCGTGTGCC	TACCTTACGC	5220
CGGCAGGCGC	GGGTAACCCG	TTGAACCCCA	TTCGTGATGG	GGATCGGGGA	TTGCAATTAT	5280
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GGTACGGCCC	CGCCGGGGTC	GGCCACCGCG	CCTGGCGGAG	CGCTGAGAAG	ACGGTCGAAC	5460
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GCGCCCCGCG	CCGTGGGGGC	GGGAACCCCC	GGGCGCCTGT	GGGGTGGTGT	CCGCGCTCGC	6420
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CCGGTCCCGT	TTGCTGTCTC	GTCTGGCCGG	CCTGAGGCAA	CCCCCTCTCC	TCTTGGGCGG	6540
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CCCTCGCCAA	ATCGACCTCG	TACGACTCTT	AGCGGTGGAT	CACTCGGCTC	GTGCGTCGAT	6660
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CCGATCAATC	GCCCCGGGGG	TGCTTCCGGG	CTCCTCGGGG	TGCGCGGCTG	GGGGTTCCCT	6840
GCGAGGGCCC	CGCGGGGGCC	CTCCGTCCCC	CTAAGCGCAG	ACCCGGCGGC	GTCCGCCCTC	6900
CTCTTGCCGC	CGCGCCCGCC	CCTTCCCCCT	CCCCCGCGCG	GCCCTGCGTG	GTCACGCGTC	6960
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TACGCGCGCG	CGCCCGCCCG	CCC CGGCTCGC	CTCGCGGCGC	GTGCGCCGGG	GCCGGGAGCC	7500
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GTGCGCCCGT	CGGGCCCGGG	GGAGGTTCTC	TCGGGGCCAC	GCGCGCGTCC	CCC GAAGAGG	9180
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TCCAGTCCGC	CGAGGGCGCA	CCACCGGCC	GTCTCGCCCG	CCGCGCCGGG	GAGGTGGAGC	9420
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CCCCCGCCCC	ACCCGCGCGC	GCCGCTCGCT	CCCTCCCCAC	CCCGCGCCCT	CTCTCTCTCT	10980
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GCGAGCCGGG	CCCTTCCCGT	GGATCGCCCC	AGCTGCGGCG	GGCGTCGCGG	CCGCCCCCGG	11220

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GTGAGACCAG	ATGTATTAAC	TCAGGCCGGG	TGCTGGTGGC	TCACGCCTGT	AACCCCAACA	36300
CTTTGGGAGG	CCGAGGCCGT	AGGATCCCTC	GAGGAATCGC	CTAACCTTGG	GGAGGTTGAG	36360
GTTGCAGTGA	GTGAGCCATA	GTTGTGTAC	TGTGCTCCAG	TCTGGGCGAA	AGACAGAATG	36420
AGGCCCTGCC	ACAGGCAGGC	AGGCAGGCAG	GCAGGCAGAA	AGACAACAGC	TGTATTATGT	36480
TCTTCTCAGG	GTAGGAAGCA	AAAATAACAG	AATACAGCAC	TTAATTAATT	TTTTTTTTTT	36540
CCTTCGGACG	GAGTTTCACT	CCTGGTGCCC	ACGCTGGAGT	GCAGTGGCAC	CATCTCGGCT	36600
CACCGCAACC	TCCACCTCCC	GCGTTCAAGC	GATTCTCCTG	CCTCAGCCTC	CTGAGTAGCT	36660
GGGATTACAG	GGAGGAGCCA	GCACACCCAG	CTGATTTTGT	ATTGTTAGTA	GAGACGGCAT	36720
TTCTCCATGT	GGGTCAGGCT	GGTCTCGAAC	TGGCGACCCC	AGTGGATCTG	CCCGCCCCGG	36780
CCTCCCAAAG	TGCTGGGGTG	ACAGGCGTGA	GCCATCGTGA	CTGGCCGGCT	ACGTTTATTT	36840
ATTTATTTTT	TTAATTATTT	TACTTTTTTT	TAGTTTTTCA	TTTTAATCTA	TTTATTTATT	36900
TACATTTATT	TATTTATTTA	TTTATTTACT	TATTTATTTA	TTTTTCGAGAC	AGACTCTCGC	36960
TCTGCTGCCC	AGGCTGGAGT	GCAGCGGCGT	GATCTCGGCT	CACTGCAACG	TCCGCCCTCCC	37020
GGGTTACACG	CATTCTCCTG	CCTCAGCCTC	CCAAGTAGCT	GGGACTACAG	GCGCCCCGCA	37080
CCGTGCCCCG	CTAACTTTTT	GTATTTTGAG	TAGAGATGGG	GTTTCACTGT	GGTAGCCAGG	37140
ATGGTCTCGA	TCTCCTGACC	CCGTGATCCG	TCCACCTCGG	CCTCCCAAAG	TGCTGGGATG	37200
ACAGGCGTGA	GCCACCGGCC	CCGCGCTATT	TATCTATTTA	TTAACTTTGA	GTCCAGGTTA	37260
TGAAACCAGT	TAGTTTTTGT	AAATTTTTTT	TTTTTTTTTT	TTTTTTTGAGA	CGAGGTTTCA	37320
CCGTGTTGCC	AAGGCTTGGA	CCGAGGGATC	CACCGGCCCT	CGGCCTCCCA	AAAGTGCGGG	37380
GATGACAGGC	GCGAGCCTAC	GCGCCCCGGA	CCCCCCTTTT	CCCCCTCCCC	CGCTTGCTCT	37440
CCCGACAGAC	AGTTTCACGG	CAGAGCGTTT	GGCTGGCGTG	CTTAAACTCA	TTCTAAATAG	37500
AAATTTGGGA	CGTCAGCTTC	TGGCCTCACG	GACTCTGAGC	CGAGGAGTCC	CCTGGTCTGT	37560
CTATCACAGG	ACCGTACACG	TAAGGAGGAG	AAAAATCGTA	ACGTTCAAAG	TCAGTCATTT	37620
TGTGATACAG	AAATACACGG	ATTACCCCAA	AACACAGAAA	CCAGTCTTTT	AGAAATGGCC	37680
TTAGCCCTGG	TGTCGGTGCC	AGTGATTCTT	TTCGGTTTGG	ACCTTGACTG	AGAGGATTCC	37740
CAGTCGGTCT	CTCGTCTCTG	GACGGAAGTT	CCAGATGATC	CGATGGGTGG	GGGACTTAGG	37800
CTGCGTCCCC	CCAGGAGCCC	TGGTCGATTA	GTTGTGGGGA	TCGCCTTGGA	GGGCGCGGTG	37860
ACCCACTGTG	CTGTGGGAGC	CTCCATCCTT	CCCCCACCCC	CCTCCCCAGG	GGGATCCCAA	37920
TTCAATCCCG	GCTGACACGC	TCACTGGCAG	GCGTCGGGGA	TCACCTAGCG	GTCAC'TGTTA	37980
CTCTGAAAAA	GGAGGCCCTCA	CAGAGGAAGG	GAGCACCAGG	CCGCCTGCGC	ACAGCTTGGG	38040
GCAACTGTGT	CTTCTCCACC	GCCCCCGCCC	CCACCTCCAA	GTTCTCTCCT	CCCTTGTTCG	38100
CTAGGAAATC	GCCACTTTGA	CGACCGGGTC	TGATTGACCT	TTGATCAGGC	AAAAACGAAC	38160
AAACAGATAA	ATAAATAAAA	TAACACAAAA	GTAACAACT	AAATAAAATA	AGTCAATACA	38220
ACCCATTACA	ATACAATAAG	ATACGATACG	ATAGGATGCG	ATAGGATACG	ATAGGATACA	38280
ATACAATAGG	ATACGATACA	ATACAATACA	ATACAATACA	ATACAATACA	ATACAATACA	38340
ATACAATAGG	ATACAATACG	CCGGGCGCGG	TGGCTCATGC	CTGTCATCCC	GTCAC'TTTGG	38400
GATGCCGAGG	TGGACGCATC	ACCTGAAGTC	GGGAGTTGGA	GACAAGCCCC	ACCAACATGG	38460
AGAAATCCCC	TCTCAATTGA	AAATACAAAA	CTAGCCGGGC	GCGGTGGCAC	ATGCCTATAA	38520

TCCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTGAGCCGA	GATTGCGCCA	TCGCACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCCGTCTC	38640
AAAAATAAAT	ACATAAAATA	ATACATACAT	ACATACATAC	ATACATACAT	ACATACATAC	38700
ATAAAATAAA	ATAAAATAAT	AAAATAAAAT	AAATAAATGG	GCCCTGCGCG	GTGGCTCAAG	38760
CCTGTCAATC	CCTCACTTTG	GGAGGCCAAG	GCCGGTGGAT	CAAGAGGCGG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAAACC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTCTGTA	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAATC	38940
GCTTGAACCT	GGGAGGCGGA	GGTTGCAGTG	AGCCGAGATC	GCGCCACTGC	AACCCAGCCT	39000
GGGCGACAGA	GCGAGACTCC	GTCTCCAAAA	AATGAAAATG	AAAATGAAAC	GCAACAAAAT	39060
AATTAAAAAG	TGAGTTTCTG	GGGAAAAAGA	AGAAAAGAAA	AAAGAAAAAA	ACAACAAAAC	39120
AGAACAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TTCGAGGCCT	CAAAACACGT	39180
AGGAATTATG	CTGTATTTCT	TTTTTTAACT	TCATTTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCGATTGT	TCTTCTCCTT	GGTCAGGGGT	TTCCTTGTCT	TTCTTCGTGT	39360
CTTTAACCCG	CGTGGACTCT	TCCGCCTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTTGT	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCAG	GATGATTGCC	39480
TTGCCTGGCC	TTGCCCTGGC	TTGCCCTTTT	TTTCTTTCTT	TCTTTCTTTA	TTACTTTCTC	39540
TTTTTCTTCT	TCTTCTTCTT	CTTTTTTTTT	AGACAGAGTT	TCACTCTTGT	TGCCCAGGCT	39600
AGAGGGCAAT	GGCGCGATCT	CGGCTCACC	CACCCCTCCG	CTCCAGGTT	CAAGCGATT	39660
TCCTGCCTCA	GCCTCCTGAT	TAGCTGGGAT	TACAGGCATG	GGCCACCGTG	CTGGCTGATG	39720
TTTGTACTTT	TAGTAGAGAC	GGTGTTTTTT	CATGTTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTT	GTCCGCCTGC	CTTAGCCTCC	CAAAGTGCTG	GGATGACAGG	CGTGCAACCG	39840
CGCCAGCCT	CTCTCTCTCT	CTCTCTCTCT	CTCGCTCGCT	TGCTTGCTTG	CTTTCGTGCT	39900
TTCTTGCTTT	CCCGTTTCTT	TGCTTCTTCT	CTTCTTCTCG	TTTCTTTCAT	GCTTGCTTTC	39960
TTGCTTGCTT	GCTTGCTTTC	GTGCTTCTCT	GCTTCTCTGT	TTTCTTCTCT	TCTTCTTCTC	40020
TTTCTTCTCT	TTGTTTCTTT	CTTGTGCTGT	TTCTTGCTTG	CTTGCTTGCT	TTCTTGCTTT	40080
TTTGCTTTCC	TGTTTCTTCT	CTTCTTCTCT	TTCTTCTTCT	TCTTCTTCTG	TTGCTTCTCT	40140
GCTTGCTTGC	TTTCGTGCTT	TCTTGTTTTT	TCGATTTCTT	TCTTCTTCTT	GTTTCTTCTC	40200
TGCTTGCTTT	CTTGCTTGCT	TGCTTCTGCT	CTTCTTGCTT	TCCTGTTTTT	TTTCTTCTCT	40260
TCTTCTTCTT	GTTTCTTCTT	TGCTTGCTTT	CTTGCTTGCT	TGCTTCTGCT	CTGCTTCTGT	40320
TCTCGATTTT	TTTCTTCTTT	TTGTTTCTTT	CCTGCTTGCT	TTCTTGCTTG	ATTGCTTCTG	40380
TGCTTCTTCT	CTTCTTCTGT	TTCTTCTTCT	CTTTTGTTTT	TTTCTTCTCT	GCTTCTTCTG	40440
TTTCTTGCTT	TCTTGCTTGC	TTGCTTCTCG	GCTTCTTCTG	TTTCTTGCTT	TCTTCTTCTT	40500
GTTTCTTCTT	TGCTTGCTTT	CTTGCTTCTT	TGTTTTCTTG	CTTCTTGCTT	TGCTTGCTTT	40560
CGTGCTTCTT	TCTTGCTTTT	CTTTCTTCTT	TTTCTTCTCT	TTTCTTCTCT	TTCTTGCTTT	40620
CTTTCTTCTT	ATCATCATCT	TTCTTCTTCT	CCTTCTTCTT	TTTCTTCTCT	TCTATCTTCT	40680
TTTCTTCTCT	TCTTCTTCTT	TTTCTTCTCT	TCTTCTTGTT	TCGTCTTCTT	GAGACAGAGT	40740
TTCACTCTTG	TTTCCACGGC	TAGAGTGCAA	TGGCGCGATC	TTGGCTCACC	GCACCTTCCG	40800
CCTCCCGGGT	TCGAGCGCTT	CTCCTGCCTC	CAGCCTCCCG	ATTAGCGGGG	ATTGACAGGG	40860
AGGCACCCCC	ACGCTGGCTG	TGGCTGATGT	TTGTGTTTTT	AGTAGGCACG	CCGTGCTCTC	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACCTCC	GACCTCCTGT	GATGCGCCCA	CCTCGGCCCT	40980
TCGAAGTGCT	GGGATGACGG	GCGTGACGAC	CGTGCCCGGC	CTGTTGACTC	ATTTCGCTTT	41040
TTTATTTCTT	TCGTTTCCAC	GCGTTTACTT	ATATGTATTA	ATGTAAACGT	TTCTGTACGC	41100
TTATATGCAA	ACAACGACAA	CGTGTATCTC	TGCATTGAAT	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAAT	AGACTTCTGT	ATGATAGATG	TAGGTGTCTG	TGTTATACAA	41220
ATAAATACAC	ATCGCTCTAT	AAAGAAGGGA	TCGTGATAAA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTTATGTG	TGTAAATGAA	CCGAGCGTAC	GATGTTATCT	CTGTTTCTCT	41340
TCTTCTCTCT	CTTCGTGTTT	TTCTTCTCTT	CTTCTTCTCT	TTCTCTCTCT	CTTTAGGTTT	41400
TTCTTCTCTT	CTTCTTCTCT	TTCTTCTCTT	CTTCTGTCCT	TTTTTTCTCT	CGTGCTTTAT	41460
TTCTCTTCTG	TTCCCTGTGT	TTCTTCTCTT	TTTCTTCTCT	CTCTGTTTCT	TTTTCCCTTC	41520
TTTCTTCTGT	TTCTTCTCTC	ATTCTTCTCT	TCTTTTCTGT	TGTTTCTTTC	CTTCCCGTCT	41580
GTCTTTTAAA	AAATTGGAGT	GTTTCAGAAG	TTTACTTTGT	GTATCTACGT	TTTCTAAATT	41640
GTCTCTCTTT	TCTCCATTTT	CTTCTCTCTT	CCCTCCCTCC	CTCCCTGCTC	CCTTCCCTCC	41700
CTCCTTCCCT	TTCGCCATCT	GTCTCTTTTC	CCCACTCCCC	TCCCCCGGTC	TGTCTCTGCG	41760
TGGATTCCGG	AAGAGCCTAC	CGATTCTGCC	TCTCCGTGTG	TCTGCAGCGA	CCCCGCGACC	41820
GAGTCTTGT	GTGTTCTTTC	TCCCTCCCTC	CCTCCCTCCC	TCCCTCCCTC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCGGT	GGGTGTGCTT	CTGACTCTGT	CGCGGTCTGAG	41940
CGAGAGACGC	GTTTTGGGCA	CCGTTTGTGT	GGGTTGGGGG	CAGAGGGGCT	CGGTTTTCCG	42000
CCTCGGGAAG	AGCTTCTCGA	CTCACGGTTT	CGCTTTCGCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGATCTG	TCTCGCTGAC	GTCCGCGGCG	GTTGTCGGGC	TCCATCTGGC	GGCCGCTTTG	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGGAAGAGC	CGCGGTCTGT	AGCCCGGCTG	GCCCGGTGGC	42240
GCCAGAGCTG	TGGCCGGTCT	CTTGAGAGTC	ACAGCTCTGG	CGTGAGGTTT	TATGTGGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCGCG	GCGGGCGTGG	GGCTGCCCCG	GCCGGTCTGAC	42360
CAGCGCGCCG	TAGCTCCCGA	GGCCCGAGCC	GCGACCCGGC	GGACCCGCCG	CGCGTGCGCG	42420

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AGGCTGGGGA CGCCCTTCCC GGCCCGGTCTG CGGTCCGCTC ATCCTGGCCG TCTGAGGCGG 42480
CGGCCGAATT CGTTTCCGAG ATCCCCGTGG GGAGCCGGGG ACCGTCCCCG CCCCCTCCCC 42540
CGGGTGCCGG GGAGCGGTCC CCGGCCGGGG CCGCGGTCCC TCTGCCGCGA TCCTTTCTGG 42600
CGAGTCCCCG TGGCCAGTCG GAGAGCGCTC CCTGAGCCGG TGCGGCCCGA GAGGTCGCGC 42660
TGGCCGGCCT TCGGTCCCTC GTGTGTCCCG GTCGTAGGAG GGGCCGGCCG AAAATGCTTC 42720
CGGCTCCCCG TCTGGAGACA CCGGCCGGCC CCTGCGTGTG GCCAGGGCCG CCGGGAGGGC 42780
TCCCCGGCCC GCGCTGTCC CCGCTGTGTG CCTTGGGTTG ACCAGAGGGA CCCCAGGCGC 42840
TCCGTGTGTG GCTGCGATGG TGGCGTTTTT GGGGACAGGT GTCCGTGTCC GTGTCGCGCG 42900
TCGCCTGGGC CGGCGGCGTG GTCGGTGACG CGACCTCCCC GCCCCGGGGG AGGTATATCT 42960
TTCGCTCCGA GTCGGCAATT TTGGGCCGCC GGGTTATAT 42999

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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CTCCCGCGCG GCCCCGTGT TCGCCGTTCC CGTGGCGCGG ACAATGCGGT TGTGCGTCCA 60
CGTGTGCGTG TCCGTGCAGT GCCGTTGTGG AGTGCCTCGC TCTCCTCCTC CTCCCCGCGA 120
CGGTTCCAC GGTGGGGAC CACCGGTGAC CTCGCCCTCT TCGGGCCTGG ATCCG 175

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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GGTCTGGTGG GAATTGTTGA CCTCGCTCTC GGGTGCGGCC TTTGGGGAAC GGC GGGGTCTG 60
GTCGTGCCCG GCGCCGACG TGTGTCGGGG CCCACTTCCC GCTCGAGGGT GGC GGTGGCG 120
GCGGCGTTGG TAGTCTCCCG TGTTGCGTCT TCCCGGGCTC TTGGGGGGGG TGCCGTCGTT 180
TTCGGGGCCG GCGTTGCTTG GCTTACGCAG GCTTGGTTTG GGA CTGCCTC AGGAGTCGTG 240
GGCGGTGTGA TTCCCGCCGG TTTTGCCCTCG CGTCTGCCTG CTTTGCCCTCG GGT TTGCTTG 300
GTTCGTGTCT CGGGAGCGGT GGT TTTTTTTT TTTTTCGGGT CCCGGGGAGA GGGGTTTTTC 360
CGGGGGACGT TCCCGTCGCC CCCTGCCGCC GGTGGGTTTT CGTTTCGGGC TGTGTTGCTT 420
TCCCCTTCCC CGTTTCGCCG TCGGTTCTCC CCGGTCGGTC GGCCCTCTCC CCGGTCGGTC 480
GCCCGGCCGT GCTGCCGGAC CCCCCCTTCT GGGGGGGATG CCCGGGCACG CACGCGTCCG 540
GGCGGCCACT GTGGTCCGGG AGCTGCTCGG CAGGCGGGTG AGCCAGTTGG AGGGGCGTCA 600
TGCCCCCGCG GGCTCCCGTG GCCGACGCGG CGTGTTCTTT GGGGGGGCCT GTGCGTGCGG 660
GAAGGCTGCG CACGTTGTCT GTCCTTGCGA GGGAAAGAGG CTTTTTTTTT TTAGGGGGTC 720
GTCCTTCGTC GTCCGTCGG CGGTGGATCC GGCCT 755

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCGCG	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCG	GCCGTCTCCC	CCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	FTCACGGCGC	CCCCACGCT	CCTCCGCCTC	TCCGCCCGTG	GTTTGGACGC	360
CTGGTTCGCG	TCTCCCCGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCGGC	CGGAAGGGTT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCCT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTG	120
CGGCGACGAC	CCATTGCAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAAT	ACAGGACTCT	TTCGAGGCCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCAACGC	CCGTCCCCGC	CCCTTGCCCTC	TCGGCGCCCC	CTCGATGCTC	180

TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTTGT	TTGGTTTTCG	GAAGTGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCCTA					378

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC	CGCTCCCCGT	TCCTCCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTGCGGGG	TGGGGTCGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCCACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTTCCCCCTC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGCCGG	GCCGCCCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCCT	CAGTGCGCC	CGGGCGTCGT	CGCGCCGTCG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCC	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACATATG	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCGTC	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTATATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTTCT	CAAACCTTAA	360
ATGGGTAAAG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTGCG	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCGC				685

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCTT AACCTAACCT CTAACCCTAA
CCCTAACCTT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21